

1/13

SEQUENCE LISTING

<110> KANEKA CORPORATION

<120> NOVEL ACYLASE GENE

<130> T719. /ACYL-1

<150> JP P2002-165722

<151> 2002-06-06.

<160> 15

<210> 1

<211> 2529

<212> DNA

<213> Stenotrophomonas maltophilia

<220>

<221> CDS

<222> (126)...(2036)

<400> 1

tctacaacgg cttggcacat gtgccatcag tcctacccccc aaagagcgca gaacgcaaag 60

cctgcacaca cttcacccgc cggggcagga gtacgcttgg gactttcctg cccgagggtt 120

cgtcc atg cat gtg cgt gcc gta gca gtt gcc atc gcc ctg agc ctg tcc 170

Met His Val Arg Ala Val Ala Val Ala Ile Ala Leu Ser Leu Ser

1

5

10

15

agc acc gtg ctg gcc gcc gac acc ccg ccg atg acc ccg gac atc agc 218

Ser Thr Val Leu Ala Ala Asp Thr Pro Pro Met Thr Pro Asp Ile Ser

20

25

30

ggc aag cct ttc att gcg ccc gat gtc ggc cgc gac tac gac aag cgc			266
Gly Lys Pro Phe Ile Ala Pro Asp Val Gly Arg Asp Tyr Asp Lys Arg			
35	40	45	
gtg gtg atg gtg ccg atg cgc gac ggt acc agg ctg tac acg gtg atc			314
Val Val Met Val Pro Met Arg Asp Gly Thr Arg Leu Tyr Thr Val Ile			
50	55	60	
gtg gtg ccc aag ggc gcg cac aat gcc ccg atc ctg ctg acc cgc acg			362
Val Val Pro Lys Gly Ala His Asn Ala Pro Ile Leu Leu Thr Arg Thr			
65	70	75	
ccc tac gat gct gcc ggc cgc gcc agc cgc agc gat tcg ccg cgc atg			410
Pro Tyr Asp Ala Ala Gly Arg Ala Ser Arg Ser Asp Ser Pro Arg Met			
80	85	90	95
cgc gac ctg ctg ccg cag ggg gat gaa gtc ttc gtc gat ggc ggc tat			458
Arg Asp Leu Leu Pro Gln Gly Asp Glu Val Phe Val Asp Gly Gly Tyr			
100	105	110	
atc cgc gtg ttc cag gac atc cgg ggc aag tac ggt tcg gaa ggc gat			506
Ile Arg Val Phe Gln Asp Ile Arg Gly Lys Tyr Gly Ser Glu Gly Asp			
115	120	125	
tat gtg atg acc cgg ccg ctg cgc ggg ccg ttg aac aac acc aag gtc			554
Tyr Val Met Thr Arg Pro Leu Arg Gly Pro Leu Asn Asn Thr Lys Val			
130	135	140	
gac cac tcc acc gat gca tgg gac acc atc gac tgg ttg gtg aaa cac			602
Asp His Ser Thr Asp Ala Trp Asp Thr Ile Asp Trp Leu Val Lys His			
145	150	155	
gtg ccg gaa agc aac ggc aag gtc ggc atg ctg ggc tcg tac gaa			650
Val Pro Glu Ser Asn Gly Lys Val Gly Met Leu Gly Ser Ser Tyr Glu			

160	165	170	175	
				698
				Gly Phe Thr Val Val Met Ala Leu Thr Asp Pro His Pro Ala Leu Lys
180	185	190		
				746
				Val Ala Ala Pro Gln Ser Pro Met Val Asp Gly Trp Met Gly Asp Asp
195	200	205		
				794
				Trp Leu Asn Tyr Gly Ala Phe Arg Gln Val Asn Phe Asn Tyr Phe Ala
210	215	220		
				842
				Met Gln Thr Glu Lys Arg Gly Lys Gly Thr Pro Leu Pro Ser Leu Gly
225	230	235		
				890
				Tyr Asp Asp Tyr Ser Thr Phe Leu Arg Ile Gly Ser Ala Gly Asp Tyr
240	245	250	255	
				938
				Ala Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val
260	265	270		
				986
				Gln His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala
275	280	285		
				1034
				Val Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly
290	295	300		
				1082
				ctg tgg gac cag gaa gac atg tgg ggc gcc aac cat gcc tac cag gcg

Leu Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala			
305	310	315	
atg gaa ggc cgc gac acc ggc aat acc cac aat tac ctg gtg atg ggc	1130		
Met Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly			
320	325	330	335
ccg tgg cgg cac agc cag gtg aac tac acc ggc aac gag ctg ggt gcg	1178		
Pro Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala			
340	345	350	
ctg aag ttc gag ggc gat acc gcg ctg cag ttc cgc cgc gat gtg ctc	1226		
Leu Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu			
355	360	365	
aag ccg ttc ttc gac cag tac ctg gtg gat ggc gca ccg aag gcc gac	1274		
Lys Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp			
370	375	380	
acg ccg ccg gtg ctc atc tac aac acc ggc gaa aac cac tgg gat cgc	1322		
Thr Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg			
385	390	395	
ctg cag ggc tgg ccg cgc agt tgc gac aag ggc tgc acg gcg gcc agc	1370		
Leu Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser			
400	405	410	415
aag ccg ctg tac ctg cgt gcc ggt ggc aag ctg gcc ttc cag gca ccg	1418		
Lys Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro			
420	425	430	
gcg gcg ggt gaa ggt gat ttc gag gaa tac gtg tcc gac ccg gcc aag	1466		
Ala Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys			
435	440	445	

ccg gtg ccg ttc gtg ccg cgc ccg gtg cgt ttt ggc gac cgt gac atg			1514
Pro Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met			
450	455	460	
tgg acc acg tgg ctg gtg aag gac caa cgt ttt gtc gat ggt cgt ccg			1562
Trp Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro			
465	470	475	
gat gtg ctg acc ttc atc acc gaa ccg ctg gcc gag ccg ctg cgg atc			1610
Asp Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile			
480	485	490	495
ggc ggc gcg ccg gtg gtg cat ctg cag gcg tcc acc agt ggc acc gac			1658
Gly Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp			
500	505	510	
agc gac tgg gtg gtg aag ctg atc gac gtc tac ccg gat cag gaa gcg			1706
Ser Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala			
515	520	525	
tca acg ccg gaa atg ggt ggc tat gag ctg ccg gtg tcg ctg gcg atc			1754
Ser Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile			
530	535	540	
ttc cgt ggg cgc tat cgg gag agt ttc agc gac ccg aag ccg ctg gca			1802
Phe Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala			
545	550	555	
gcg aac cag gtg ctg ccg tac cgc ttt gat ctg ccc aat gcc aac cat			1850
Ala Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His			
560	565	570	575
gtg ttc cag aag ggg cac cgg gtg atg gtg cag gtg cag tcc agc ctg			1898
Val Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu			
580	585	590	

ttc ccg ctg tat gac cgc aac ccg cag acc tac gtg ccg aac atc tac		1946
Phe Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr		
595	600	605
ctg gcc aag ccg ggc gat tac cag aag gcc acg cag cgg gtg tgg cac		1994
Leu Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His		
610	615	620
agc gcc gcg cag gcg agc tac gtc gac ctg ccg gtg tac tga		2036
Ser Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr		
625	630	635
ggcggagaat ggcgtggtag tgccggccgc tggccggcaa cgccggagcgg tagcgccggg		2096
ccatgcccgg cggatgggt agtgccggcc gctggccggc aacgccccgtga agccggcgcg		2156
tgtcgaccaa ggccgacacc tgccagagca cgtcagccta cttcgaggg accggtgtgc		2216
cagcggctgg gaaccagacc gaagcgcttg cgaaaggcgg cggcgaagtt gctgggtgg		2276
cggtagccgg tggcgccgc cgcctgttca acgctccagc cgtgtcgcg caggccgcgt		2336
tcggcgtggt gcatgcgttg ttctgtgcagg tagtcgaaca ccgagcaccc gtattgctgc		2396
acgaagtggc ggccgcagcga gctgggactc atgcaggcca gctgggccag ttccaccagg		2456
ctgtggcgt ggctgggatc gtcgtgcagg aagcccccga cgcgttcaat cggcccaagt		2516
tggccgcgcc aaa		2529

<210> 2

<211> 636

<212> PRT

<213> Stenotrophomonas maltophilia

<400> 2

Met His Val Arg Ala Val Ala Val Ala Ile Ala Leu Ser Leu Ser Ser			
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Thr Val Leu Ala Ala Asp Thr Pro Pro Met Thr Pro Asp Ile Ser Gly			
20	25		30
Lys Pro Phe Ile Ala Pro Asp Val Gly Arg Asp Tyr Asp Lys Arg Val			
35	40	45	
Val Met Val Pro Met Arg Asp Gly Thr Arg Leu Tyr Thr Val Ile Val			
50	55	60	
Val Pro Lys Gly Ala His Asn Ala Pro Ile Leu Leu Thr Arg Thr Pro			
65	70	75	80
Tyr Asp Ala Ala Gly Arg Ala Ser Arg Ser Asp Ser Pro Arg Met Arg			
85	90	95	
Asp Leu Leu Pro Gln Gly Asp Glu Val Phe Val Asp Gly Gly Tyr Ile			
100	105	110	
Arg Val Phe Gln Asp Ile Arg Gly Lys Tyr Gly Ser Glu Gly Asp Tyr			
115	120	125	
Val Met Thr Arg Pro Leu Arg Gly Pro Leu Asn Asn Thr Lys Val Asp			
130	135	140	
His Ser Thr Asp Ala Trp Asp Thr Ile Asp Trp Leu Val Lys His Val			
145	150	155	160
Pro Glu Ser Asn Gly Lys Val Gly Met Leu Gly Ser Ser Tyr Glu Gly			
165	170	175	
Phe Thr Val Val Met Ala Leu Thr Asp Pro His Pro Ala Leu Lys Val			
180	185	190	
Ala Ala Pro Gln Ser Pro Met Val Asp Gly Trp Met Gly Asp Asp Trp			
195	200	205	
Leu Asn Tyr Gly Ala Phe Arg Gln Val Asn Phe Asn Tyr Phe Ala Met			
210	215	220	
Gln Thr Glu Lys Arg Gly Lys Gly Thr Pro Leu Pro Ser Leu Gly Tyr			
225	230	235	240
Asp Asp Tyr Ser Thr Phe Leu Arg Ile Gly Ser Ala Gly Asp Tyr Ala			
245	250	255	

Arg Phe Thr Gly Val Asp Gln Leu Thr Trp Trp Lys Lys Leu Val Gln
 260 265 270
 His Pro Ala Tyr Asp Gly Phe Trp Gln Gly Gln Ala Leu Asp Ala Val
 275 280 285
 Met Ala Lys Thr Pro Leu Lys Val Pro Thr Met Trp Leu Gln Gly Leu
 290 295 300
 Trp Asp Gln Glu Asp Met Trp Gly Ala Asn His Ala Tyr Gln Ala Met
 305 310 315 320
 Glu Gly Arg Asp Thr Gly Asn Thr His Asn Tyr Leu Val Met Gly Pro
 325 330 335
 Trp Arg His Ser Gln Val Asn Tyr Thr Gly Asn Glu Leu Gly Ala Leu
 340 345 350
 Lys Phe Glu Gly Asp Thr Ala Leu Gln Phe Arg Arg Asp Val Leu Lys
 355 360 365
 Pro Phe Phe Asp Gln Tyr Leu Val Asp Gly Ala Pro Lys Ala Asp Thr
 370 375 380
 Pro Pro Val Leu Ile Tyr Asn Thr Gly Glu Asn His Trp Asp Arg Leu
 385 390 395 400
 Gln Gly Trp Pro Arg Ser Cys Asp Lys Gly Cys Thr Ala Ala Ser Lys
 405 410 415
 Pro Leu Tyr Leu Arg Ala Gly Gly Lys Leu Ala Phe Gln Ala Pro Ala
 420 425 430
 Ala Gly Glu Gly Asp Phe Glu Glu Tyr Val Ser Asp Pro Ala Lys Pro
 435 440 445
 Val Pro Phe Val Pro Arg Pro Val Arg Phe Gly Asp Arg Asp Met Trp
 450 455 460
 Thr Thr Trp Leu Val Lys Asp Gln Arg Phe Val Asp Gly Arg Pro Asp
 465 470 475 480
 Val Leu Thr Phe Ile Thr Glu Pro Leu Ala Glu Pro Leu Arg Ile Gly
 485 490 495
 Gly Ala Pro Val Val His Leu Gln Ala Ser Thr Ser Gly Thr Asp Ser
 500 505 510
 Asp Trp Val Val Lys Leu Ile Asp Val Tyr Pro Asp Gln Glu Ala Ser
 515 520 525
 Thr Pro Glu Met Gly Gly Tyr Glu Leu Pro Val Ser Leu Ala Ile Phe

530	535	540
Arg Gly Arg Tyr Arg Glu Ser Phe Ser Asp Pro Lys Pro Leu Ala Ala		
545	550	555
Asn Gln Val Leu Pro Tyr Arg Phe Asp Leu Pro Asn Ala Asn His Val		
565	570	575
Phe Gln Lys Gly His Arg Val Met Val Gln Val Gln Ser Ser Leu Phe		
580	585	590
Pro Leu Tyr Asp Arg Asn Pro Gln Thr Tyr Val Pro Asn Ile Tyr Leu		
595	600	605
Ala Lys Pro Gly Asp Tyr Gln Lys Ala Thr Gln Arg Val Trp His Ser		
610	615	620
Ala Ala Gln Ala Ser Tyr Val Asp Leu Pro Val Tyr		
625	630	635

<210> 3
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 <212> PRT
 <213> Stenotrophomonas maltophilia

<220>
 <221> PEPTIDE
 <222> (1)...(25)

<400> 3
 Val Pro Thr Met Trp Leu Gln Gly Leu Trp Asp Gln Glu Asp Met Trp
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 Gly Ala Asn His Ala Tyr Gln Ala Met
 20 25

<210> 4
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K1 primer

<400> 4

tgggaycarg argayatgtg ggg

23

<210> 5

<211> 8

<212> PRT

<213> Stenotrophomonas maltophilia

<220>

<221> PEPTIDE

<222> (1)...(8)

<400> 5

Trp Asp Gln Glu Asp Met Trp Gly

1 5

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K-Nde I-4 primer

<400> 6

ggaattccat atgcatgtgc gtgccgtgc

30

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: K-BamH I-1 primer

<400> 7

cgcggatcct cagtacaccg gcaggtc

27

<210> 8

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-197 primer

<400> 8

aaaaagcagg ctggcacgac aggttcccg actgga

36

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MT-198 primer

<400> 9

agaaagctgg gtggatcctc agtacaccgg caggtcga

38

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: attB1 primer

<400> 10
ggggacaagt ttgtacaaaa aaggcaggct

29

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: attB2 primer

<400> 11
ggggaccact ttgtacaaga aagctgggt

29

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: MT-216 primer

<400> 12
cgccctctaga agcgattcgc cgcgcatgcg cgacc

35

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: MT-219 primer

<400> 13
gcacaagctt cttccaccag gtcagctgg

29

<210> 14
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: MT-217 primer

<400> 14
tcgcttctag aggcgccggcc ggcagcatcg tagggc

36

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: MT-218 primer

<400> 15
ggaagaagct tgtgcagcac ccggcc

26